



UTHou-16UTL final.ST25
SEQUENCE LISTING

<110> Board of Regents of the University of Texas System

<120> MUTATIONS IN A NOVEL PHOTORECEPTOR-PINEAL GENE ON 17P CAUSE LEBER CONGENITAL AMAUROSIS (LCA4)

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<140> 09/765,061
<141> 2001-01-17

<150> 60/331362
<151> 2001-01-14

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<170> PatentIn version 3.3

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<213> Pan troglodytes

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<223> The AIPL1 gene produces the aryl-hydrocarbon receptor interacting protein-like 1

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<212> DNA
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<213> Canis familiaris

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<222> (1)..(925)
<223> The AIP1 gene produces the aryl-hydrocarbon receptor interacting protein-like 1

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<213> Mus musculus

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<222> (1)..(1075)

<223> The AIPL1 gene produces the aryl-hydrocarbon receptor interacting protein-like 1

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<213> Macaca mulatta

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<222> (1)..(1179)

<223> The AIPL1 gene produces the aryl-hydrocarbon receptor interacting protein-like 1

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aatgtgatg	aggagcgcac	ggtcatcgac	gacagccgtc	aggtggacca	gccccatgcac	180
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gtgcacgagg	tggccagtt	ctggcgac	accatccaca	cgggggtcta	ccccatyctg	300
tcccggagcc	tgcggcagat	ggcccaggc	aaggaccca	cggagtggca	cgtgcacaca	360
tgcgggctgg	ccaacatgtt	cgcctaccac	acgctggct	acgaggacct	ggacgagctg	420
cagaaggagc	ctcagcctct	gatcttgtg	atcgagctgc	tgcagggtga	cgcggcagat	480
gattaccaga	gggagacctg	gaacctgagc	aatcatgaga	agatgaaggt	ggtgcggcgtc	540
ctccacggag	aggaaatcg	gctttcaag	ytggggcgt	acgaggagc	ctcttccaag	600
taccaggagg	ccatcatctg	cctaaggaac	ctgcagacca	aggagaagcc	gtgggaggtg	660
cagtggctga	agctggagaa	gatgatcaac	accctgaccc	tcaactactg	ccagtgccctg	720
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ccaggcatcg	tgaaggccta	ctatgtcgt	gccccggc	acgcggaggt	gtggAACGAG	840
gccgaggcca	aggcggaccc	ccagaaagtg	ctggagctgg	agccatccat	gcagaaggcg	900
gtgcgcagg	agctgaggct	gctggagaac	cgcattggcg	agaagcagga	ggaggagagg	960
ctgcgtgcc	ggaacatgct	gagccaggga	gccacgcagc	ctcccgac	gccaccggca	1020
cagcccccca	cagcaccacc	tgcagagctg	tccacagggc	cacctgcgga	cccaccggcg	1080
gagcccccca	cagcaccacc	tgcggagctg	tccacagggc	cacctgcaga	gccaccggca	1140
gagctcccccc	tgtccccagg	gcactcactg	cagcactga			1179

<210>	8	
<211>	1119	
<212>	DNA	
<213>	Saimiri sciureus	

<220>		
<221>	gene	
<222>	(1)..(1119)	
<223>	The AIPL1 gene produces the aryl-hydrocarbon receptor interacting protein-like 1	

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aaatgtgatg	aggagcggac	ggtgattgac	gacagcaggg	aggtgggcca	gccccatgcac	180
atcatcatcg	ggaacatgtt	caagctggag	gtctggaga	tcctgctcac	gtcccatgcgg	240
gtgcgagagg	tggccgagtt	ctgggtgcac	accatccaca	cgggggtcta	ccccatcctg	300
tcccggagcc	tgcggcagat	ggcccagggc	aaggacccga	cggagtggca	tgtgcacacg	360
tgcgggctgg	ccaacatgtt	cgcctaccac	acgctgggct	acgaggacct	ggatgagctg	420
cagaaggagc	ctcagcctct	gatctttgtg	atcgagctgc	tgcaggttga	tgccccaaagt	480
Gattaccaga	gggagacctg	gaacctgagc	aatcacfagaga	agatgaaggt	ggtgcccgctc	540
ctccatggag	aaggaaatag	gctcttcaag	ctggggccgct	acgaggaggc	ctcttccaag	600
taccaggagg	ccatcatctg	cctaaggaac	ctgcagacca	aggagaaacc	ctgggaggtg	660
cagtggctga	agctggagaa	gatgatcaat	accctgatcc	tcaactactg	tcagtgtctg	720
ctgaagaagg	aggagtacta	cgaggtcctg	gagcatacca	gtgacattct	ccggcaccac	780
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gccgaggcca	aggcggacct	ccagaaaagtg	ctggagctgg	agccgtccat	gcagaaggcg	900
gtgcgcaggg	agctgaggct	gctggagaac	cgcattggcg	agaacgagga	ggaggagcgg	960
ctgcgcgtgcc	gcaacatgct	gagccagggg	gccacgtgg	cccccgccga	gccacccgca	1020
gagccacctg	cagactcatc	cacagagcca	cccgccagac	cacctgcaga	gccacctgca	1080
gagctaacct	tgaccccggg	gcacccacta	cagcactga			1119

<210> 9
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<213> Homo sapiens

<220>
<221> mutation
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<223> Amino Acid codon position 79: Met to Thr mutation

<400> 9
acctccacgc ggggtg 15

<210> 10
<211> 15
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (7)..(9)

UTHou-16UTL final.ST25

<223> Amino Acid codon 88 mutation: Trp to X

<400> 10

gagttctgat gcgac

15

<210> 11

<211> 15

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (7)..(9)

<223> Amino Acid codon 96 mutation: Val to Ile mutation

<400> 11

acggggatct acccc

15

<210> 12

<211> 15

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (7)..(9)

<223> Amino Acid codon 124 mutation: Thr to Ile mutation

<400> 12

gaccccatag agtgg

15

<210> 13

<211> 15

<212> DNA

<213> Homo sapiens

<220>

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<223> Amino Acid codon 376 mutation: Pro to Ser mutation

<400> 13

ccaccctcgt cccca

15

<210> 14

<211> 15

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

UTHou-16UTL final.ST25
<222> (7)..(9)
<223> Amino Acid codon 163 mutation: Gln to X mutation

<400> 14
gattactaga gggag

15

<210> 15
<211> 15
<212> DNA
<213> Homo sapiens

<220>
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<222> (7)..(9)
<223> Amino Acid codon 197 mutation: Ala to Pro mutation

<400> 15
gaggagccct cttcc

15

<210> 16
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<212> DNA
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<220>
<221> mutation
<222> (7)..(9)
<223> Amino Acid codon 278 mutation: Trp to X mutation

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gaggtgtgaa atgag

15

<210> 17
<211> 15
<212> DNA
<213> Homo sapiens

<220>
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<222> (7)..(7)
<223> a to g mutation: IVS2-2A to G

<400> 17
tccccacggc acacg

15

<210> 18
<211> 15
<212> DNA
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<220>

UTHou-16UTL final.ST25

<221> mutation
<222> (7)..(9)
<223> Amino Acid codon 262 mutation: Glu to Ser

<400> 18
cacccaagtgcgcgg

15

<210> 19
<211> 15
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (7)..(9)
<223> Amino Acid codon 302 mutation: Arg to Leu

<400> 19
gcggtgctca gggag

15

<210> 20
<211> 13
<212> DNA
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<220>
<221> mutation
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<223> Deletion of "tgcagagccacc" at location 5

<400> 20
gccacccaca gca

13

<210> 21
<211> 15
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
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<223> Amino Acid codon 239 mutation: Cys to Arg

<400> 21
tgccagcgcc tgctg

15

<210> 22
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<212> DNA
<213> Homo sapiens

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<220>
<221> mutation
<222> (5)..(5)
<223> two base deletion at location 5: "ag"

<400> 22
tccccgagcc acc

13

<210> 23
<211> 15
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (7)..(9)
<223> Amino Acid codon 42 mutation: Cys to X

<400> 23
atgaaatgag atgag

15

<210> 24
<211> 12
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (7)..(7)
<223> nine base deletion at location 7: "ctccggcac"

<400> 24
gatattcacc ca

12

<210> 25
<211> 21
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (7)..(7)
<223> eight base insertion: "gtgatctt"

<400> 25
gacttaggtga tcttgtgatc t

21

<210> 26
<211> 12
<212> DNA
<213> Homo sapiens

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<220>
<221> mutation
<222> (4)..(4)
<223> g to a polymorphism: IVS1-9 g to a benign mutation

<400> 26
ctcagtgact ag

12

<210> 27
<211> 12
<212> DNA
<213> Homo sapiens

<220>
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<222> (4)..(4)
<223> g to c polymorphism: IVS2+66G to C Benign

<400> 27
tttgccgggc tg

12

<210> 28
<211> 12
<212> DNA
<213> Homo sapiens

<220>
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<222> (4)..(4)
<223> c to t polymorphism: IVS2-88C to T Benign

<400> 28
tcctctcagg ag

12

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<211> 12
<212> DNA
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<220>
<221> mutation
<222> (4)..(4)
<223> g to a polymorphism: IVS2-14G to A Benign

<400> 29
atccatttat cc

12

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<220>
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<222> (4)..(4)
<223> a to c mutation: IVS2-10A to C Benign

<400> 30
cgtttctccc ca

12

<210> 31
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<212> DNA
<213> Homo sapiens

<220>
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<400> 31
ctgccccact ga

12

<210> 32
<211> 12
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<220>
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<223> t to c mutation: IVS3-21T to C Benign

<400> 32
cctcaccgac ct

12

<210> 33
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<212> DNA
<213> Homo sapiens

<220>
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<222> (7)..(7)
<223> g to a mutation: IVS5+18G to A Benign

<400> 33
aggagcggac ag

12

<210> 34
<211> 12
<212> DNA

UTHou-16UTL final.ST25

<213> Homo sapiens

<220>
<221> mutation
<222> (7)..(9)
<223> Amino Acid codon mutation: Asp 90 His Benign

<400> 34
tggtgccaca cc

12

<210> 35
<211> 12
<212> DNA
<213> Homo sapiens

<220>
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<222> (4)..(6)
<223> Amino Acid mutation: Phe 37 Phe Benign

<400> 35
catttccgca cc

12

<210> 36
<211> 12
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (4)..(6)
<223> Amino Acid mutation: Ser 78 Ser Benign

<400> 36
acctcttatgc gg

12

<210> 37
<211> 12
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<220>
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<222> (4)..(6)
<223> Amino Acid mutation: Cys 89 Cys Benign

<400> 37
tggtgtgaca cc

12

<210> 38
<211> 12

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<212> DNA
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<220>
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<223> Amino Acid codon mutation: Leu 100 Leu Benign

<400> 38
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12

<210> 39
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<212> DNA
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<220>
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<222> (4)..(6)
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<400> 39
aatcacgaga ag

12

<210> 40
<211> 12
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (4)..(6)
<223> Amino Acid codon mutation: Pro 217 Pro Benign

<400> 40
aagccgtggg ag

12

<210> 41
<211> 12
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (4)..(6)
<223> Amino Acid codon mutation: Asp 255 Asp Benign

<400> 41
agtgacattc tc

12

<210> 42

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<211> 20
<212> DNA
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<220>
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<222> (1)..(20)
<223> PCR primer 1 page 57

<400> 42
aagaaaaacca ttctgcacgg

20

<210> 43
<211> 19
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(19)
<223> PCR primer 2 page 57

<400> 43
tgcagtcgt ccaggtcct

19

<210> 44
<211> 17
<212> DNA
<213> Homo sapiens

<220>
<221> primer
<222> (1)..(17)
<223> PCR primer 1 page 58

<400> 44
gacacctccc tttctcc

17

<210> 45
<211> 18
<212> DNA
<213> Homo sapiens

<400> 45
gctggggctg cctggctg

18

<210> 46
<211> 20
<212> DNA
<213> Homo sapiens

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<220>
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<222> (1)..(20)
<223> PCR primer 3 page 58

<400> 46
ccgagtgatt accagaggga

20

<210> 47
<211> 20
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(20)
<223> PCR primer 4 page 58

<400> 47
tgagctccag cacctcatag

20

<210> 48
<211> 18
<212> DNA
<213> Homo sapiens

<220>
<221> primer
<222> (1)..(18)
<223> PCR primer 1 page 60

<400> 48
acgcagaggt gtggatg

18

<210> 49
<211> 19
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(19)
<223> PCR primer 2 page 60

<400> 49
aaaaagtgac accacgatc

19

<210> 50
<211> 34
<212> DNA
<213> Homo sapiens

UTHou-16UTL final.ST25

<220>
<221> exon
<222> (1)..(34)
<223> exon - donor splice site 1 of Table 1 page 49
CGGATCCCGAgtgagtggggccctccggagcaga

<400> 50
cgg atc ccg agt gag tgg ggc cct ccg gag cag a 34
Arg Ile Pro Ser Glu Trp Gly Pro Pro Glu Gln
1 5 10

<210> 51
<211> 35
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> (1)..(35)
<223> exon - acceptor splice site 1 of Table 1 page 49
cagagtgcaccgtctcggtgactagGTGATCTTC

<400> 51
cag agt gca ccg tct cgg tga cta ggt gat ctt tc 35
Gln Ser Ala Pro Ser Arg Leu Gly Asp Leu
1 5 10

<210> 52
<211> 35
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> (1)..(35)
<223> exon - donor splice site 2 of Table 1 page 49
CSACACCATCgtaagttaggcctgcgcgcgtct

<400> 52
csa cac cat cgt aag tag gcc ctg cgc gcc tgt ct 35
Xaa His His Arg Lys Ala Leu Arg Ala Cys
1 5 10

<210> 53
<211> 35
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> (1)..(35)

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<223> exon - acceptor splice site 2 of Table 1 page 49
      gccatccatccgttatccccacagCACACGGGGG

<400> 53
      gcc atc cat ccg ttt atc ccc aca gca cac ggg gg
      Ala Ile His Pro Phe Ile Pro Thr Ala His Gly
      1           5           10

      35

<210> 54
<211> 35
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(35)
<223> exon - donor splice site 3 of Table 1 page 49
      GCTGCTGCAGgtggggctggggttggcaggcgtgg

<400> 54
      gct gct gca ggt ggg gct ggg gtt ggc agg gct gg
      Ala Ala Ala Gly Gly Ala Gly Val Gly Arg Ala
      1           5           10

      35

<210> 55
<211> 35
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> (1)..(35)
<223> exon - acceptor splice site 3 of Table 1 page 49
      cactgacctgcagctctggggccagGTTGATGCC

<400> 55
      cac tga cct gca gct ctg ggg cca ggt tga tgc cc
      His     Pro Ala Ala Leu Gly Pro Gly     Cys
      1           5

      35

<210> 56
<211> 35
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> (1)..(35)
<223> exon - donor splice site 4 of Table 1 page 49

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GCAGACCAAGgtcagaggccgctggcacggggtg

<400> 56

gca gac caa ggt cag agg ccg ctg gcc acg ggg tg
Ala Asp Gln Gly Gln Arg Pro Leu Ala Thr Gly
1 5 10

35

<210> 57

<211> 35

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (1)..(35)

<223> exon - acceptor splice site 4 of Table 1 page 49

catggctgaccttctccctgggcagGAGAAGCCRT

<400> 57

cat ggc tga cct tct ccc tgg gca gga gaa gcc rt
His Gly Pro Ser Pro Trp Ala Gly Glu Ala
1 5 10

35

<210> 58

<211> 35

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (1)..(35)

<223> exon - donor splice site 5 of Table 1 page 49

CACCACCCAGgtgcgcgggctgcagggcgacaca

<400> 58

cac cac cca ggt gcg cggt ggc tgc agg ggc gga ca
His His Pro Gly Ala Arg Gly Cys Arg Gly Gly
1 5 10

35

<210> 59

<211> 35

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (1)..(35)

<223> exon - acceptor splice site 5 of Table 1 page 49

gctggatgctccctgctccccacagGCATCGTGAA

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<400> 59
gct gga tgc tcc ctg ctc ccc aca ggc atc gtg aa 35
Ala Gly Cys Ser Leu Leu Pro Thr Gly Ile Val
1 5 10

<210> 60
<211> 18
<212> DNA
<213> *Homo sapiens*

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<220>
<221> primer
<222> (1)..(18)
<223> PCR Primer 1 for AIPL1 fragment amplification Table 5 page 61
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<400> 60
ggacacctcc ctttctcc 18

<210> 61
<211> 18
<212> DNA
<213> *Homo sapiens*

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<220>
<221> primer
<222> (1)..(18)
<223> PCR Primer 2 for AIPL1 fragment amplification Table 5 page 61
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<400> 61
gctggggctg cctggctg 18

<210> 62
<211> 20
<212> DNA
<213> *Homo sapiens*

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<220>
<221> primer
<222> (1)..(20)
<223> PCR Primer 3 for AIPL1 fragment amplification Table 5 page 61
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<400> 62
gggccttgaa cagtgtgtct 20

<210> 63
<211> 19
<212> DNA
<213> *Homo sapiens*

<220>
<221> primer

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<222> (1)..(19)
<223> PCR Primer 4 for AIPL1 fragment amplification Table 5 page 61

<400> 63
tttcccgaaa cacagcagc 19

<210> 64
<211> 18
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(18)
<223> PCR Primer 5 for AIPL1 fragment amplification Table 5 page 61

<400> 64
agtgagggag caggattc 18

<210> 65
<211> 20
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(20)
<223> PCR Primer 6 for AIPL1 fragment amplification Table 5 page 61

<400> 65
tgcccatgtat gccccgtgtc 20

<210> 66
<211> 18
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(18)
<223> PCR Primer 7 for AIPL1 fragment amplification Table 5 page 61

<400> 66
tttcgggtct ctgatggg 18

<210> 67
<211> 17
<212> DNA
<213> Homo sapiens

<220>

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<221> primer
<222> (1)..(17)
<223> PCR Primer 8 for AIPL1 fragment amplification Table 5 page 61

<400> 67

gcaggctccc cagagtc

17

<210> 68
<211> 19
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(19)
<223> PCR Primer 9 for AIPL1 fragment amplification Table 5 page 61

<400> 68

gcagctgcct caggtcatg

19

<210> 69
<211> 18
<212> DNA
<213> Homo sapiens

<220>
<221> primer
<222> (1)..(18)
<223> PCR Primer 10 for AIPL1 fragment amplification Table 5 page 61

<400> 69

gtggggtgga aagaaaag

18

<210> 70
<211> 18
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(18)
<223> PCR Primer 11 for AIPL1 fragment amplification Table 5 page 61

<400> 70

ctgggaaggg agctgtag

18

<210> 71
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<212> DNA
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<220>
<221> primer
<222> (1)..(19)
<223> PCR Primer 12 for AIPL1 fragment amplification Table 5 page 61

<400> 71
aaaagtgaca ccacgatcc 19

<210> 72
<211> 384
<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE
<222> (1)..(384)
<223> Human AIPL1 Protein

<400> 72

Met Asp Ala Ala Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile
1 5 10 15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg
20 25 30

Val Ile Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val
35 40 45

Ile Asp Asp Ser Arg Gln Val Gly Gln Pro Met His Ile Ile Ile Gly
50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu Leu Thr Ser Met Arg
65 70 75 80

Val His Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val
85 90 95

Tyr Pro Ile Leu Ser Arg Ser Leu Arg Gln Met Ala Gln Gly Lys Asp
100 105 110

Pro Thr Glu Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala
115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro
130 135 140

Gln Pro Leu Val Phe Val Ile Glu Leu Leu Gln Val Asp Ala Pro Ser
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145 150 155 160
Asp Tyr Gln Arg Glu Thr Trp Asn Leu Ser Asn His Glu Lys Met Lys
165 170 175

Ala Val Pro Val Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly
180 185 190

Arg Tyr Glu Glu Ala Ser Ser Lys Tyr Gln Glu Ala Ile Ile Cys Leu
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys
210 215 220

Leu Glu Lys Met Ile Asn Thr Leu Ile Leu Asn Tyr Cys Gln Cys Leu
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg Ala Arg
260 265 270

Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala Asp Leu Gln
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Gln Lys Ala Val Arg Arg Glu
290 295 300

Leu Arg Leu Leu Glu Asn Arg Met Ala Glu Lys Gln Glu Glu Glu Arg
305 310 315 320

Leu Xaa Cys Arg Asn Met Leu Ser Gln Gly Ala Thr Gln Pro Pro Ala
325 330 335

Glu Pro Pro Thr Glu Pro Pro Ala Gln Ser Ser Thr Glu Pro Pro Ala
340 345 350

Glu Pro Pro Thr Ala Pro Ser Ala Glu Leu Ser Ala Gly Pro Pro Ala
355 360 365

Glu Pro Ala Thr Glu Pro Pro Ser Pro Gly His Ser Leu Gln His
370 375 380

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<210> 73
<211> 384
<212> PRT
<213> Pan troglodytes

<220>
<221> Peptide
<222> (1)..(384)
<223> Chimpanzee AIPL1 Protein

<400> 73

Met Asp Ala Ala Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile
1 5 10 15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg
20 25 30

Val Ile Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val
35 40 45

Ile Asp Asp Ser Arg Gln Val Gly Gln Pro Met His Ile Ile Ile Gly
50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu Leu Thr Ser Met Arg
65 70 75 80

Val His Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val
85 90 95

Tyr Pro Ile Leu Ser Arg Ser Leu Arg Gln Met Ala Gln Gly Lys Asp
100 105 110

Pro Thr Glu Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala
115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro
130 135 140

Gln Pro Leu Val Phe Val Ile Glu Leu Leu Gln Val Asp Ala Pro Ser
145 150 155 160

Asp Tyr Gln Arg Glu Thr Trp Asn Leu Ser Asn His Glu Lys Met Lys
165 170 175

Ala Val Pro Val Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly
180 185 190

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Arg Tyr Glu Glu Ala Ser Ser Lys Tyr Gln Glu Ala Ile Ile Cys Leu
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys
210 215 220

Leu Glu Lys Met Ile Asn Thr Leu Ile Leu Asn Tyr Cys Gln Cys Leu
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg Ala Arg
260 265 270

Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala Asp Leu Arg
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Gln Lys Ala Val Arg Arg Glu
290 295 300

Leu Arg Leu Leu Glu Asn Arg Met Ala Glu Lys Gln Glu Glu Glu Arg
305 310 315 320

Leu Arg Cys Arg Asn Met Leu Ser Gln Gly Ala Thr Gln Pro Pro Ala
325 330 335

Glu Pro Pro Thr Glu Pro Pro Ala Gln Ser Ser Thr Glu Pro Pro Ala
340 345 350

Glu Pro Pro Pro Ala Pro Ser Ala Glu Leu Ser Ala Gly Pro Pro Ala
355 360 365

Glu Thr Ala Thr Glu Pro Pro Pro Ser Pro Gly His Ser Leu Gln His
370 375 380

<210> 74
<211> 372
<212> PRT
<213> Papio anubis

<220>
<221> peptide
<222> (1)..(372)

UTHou-16UTL final.ST25

<223> Baboon AIPL1 Protein

<400> 74

Met Asp Ala Ala Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile
1 5 10 15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg
20 25 30

Val Ile Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val
35 40 45

Ile Asp Asp Ser Arg Gln Val Asp Gln Pro Met His Ile Ile Ile Gly
50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu Leu Thr Ser Met Arg
65 70 75 80

Val His Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val
85 90 95

Tyr Pro Ile Leu Ser Arg Ser Leu Arg Gln Met Ala Gln Gly Lys Asp
100 105 110

Pro Thr Glu Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala
115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro
130 135 140

Gln Pro Leu Ile Phe Val Ile Glu Leu Leu Gln Val Asp Ala Pro Ser
145 150 155 160

Asp Tyr Gln Arg Glu Thr Trp Asn Leu Ser Asn His Glu Lys Met Lys
165 170 175

Val Val Pro Val Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly
180 185 190

Arg Tyr Glu Glu Ala Ser Ser Lys Tyr Gln Glu Ala Ile Ile Cys Leu
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys
210 215 220

UTHou-16UTL final.ST25

Leu Glu Lys Met Ile Asn Thr Leu Thr Leu Asn Tyr Cys Gln Cys Leu
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg Ala Arg
260 265 270

Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala Asp Leu Gln
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Gln Lys Ala Val Arg Arg Glu
290 295 300

Leu Arg Leu Leu Glu Asn Arg Met Ala Glu Lys Gln Glu Glu Glu Arg
305 310 315 320

Leu Arg Cys Arg Asn Met Leu Ser Gln Gly Ala Thr Gln Pro Pro Thr
325 330 335

Glu Pro Pro Ala Glu Pro His Thr Ala Pro Pro Ala Glu Leu Ser Thr
340 345 350

Gly Pro Pro Ala Glu Pro Pro Ala Glu Leu Pro Leu Ser Pro Gly His
355 360 365

Ser Leu Gln His
370

<210> 75
<211> 328
<212> PRT
<213> Bos taurus

<400> 75

Met Asp Ala Thr Leu Leu Leu Asn Val Glu Gly Ile Lys Lys Thr Ile
1 5 10 15

Leu His Gly Gly Thr Gly Asp Leu Pro Asn Phe Ile Thr Gly Ala Arg
20 25 30

Val Thr Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val
35 40 45

UTHou-16UTL final.ST25

Ile Asp Asp Ser Lys Gln Val Gly His Pro Met His Ile Ile Ile Gly
50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu Leu Thr Ser Met Arg
65 70 75 80

Val Ser Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val
85 90 95

Tyr Pro Ile Leu Ser Arg Ser Leu Arg Gln Met Ala Glu Gly Lys Asp
100 105 110

Pro Thr Glu Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala
115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro
130 135 140

Gln Pro Leu Ile Phe Ile Ile Glu Leu Leu Gln Val Glu Ala Pro Ser
145 150 155 160

Gln Tyr Gln Arg Glu Thr Trp Asn Leu Asn Asn Gln Glu Lys Met Gln
165 170 175

Ala Val Pro Ile Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly
180 185 190

Arg Tyr Glu Glu Ala Ser Asn Lys Tyr Gln Glu Ala Ile Val Cys Leu
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys
210 215 220

Leu Glu Lys Met Ile Asn Thr Leu Ile Leu Asn Tyr Cys Gln Cys Leu
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg Ala Arg
260 265 270

Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala Asp Leu Glu
275 280 285

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Lys Val Leu Glu Leu Glu Pro Ser Met Arg Lys Ala Val Gln Arg Glu
290 295 300

Leu Arg Leu Leu Glu Asn Arg Leu Glu Glu Lys Arg Glu Glu Glu Arg
305 310 315 320

Leu Arg Cys Arg Asn Met Leu Gly
325

<210> 76
<211> 328
<212> PRT
<213> Mus musculus

<220>
<221> peptide
<222> (1)..(328)
<223> Mouse AIPL1 Protein

<400> 76

Met Asp Val Ser Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile
1 5 10 15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg
20 25 30

Val Thr Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val
35 40 45

Ile Asp Asp Ser Lys Gln Val Gly Gln Pro Met Ser Ile Ile Ile Gly
50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Thr Leu Leu Thr Ser Met Arg
65 70 75 80

Leu Gly Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val
85 90 95

Tyr Pro Met Leu Ser Arg Ser Leu Arg Gln Val Ala Glu Gly Lys Asp
100 105 110

Pro Thr Ser Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala
115 120 125

UTHou-16UTL final.ST25

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro
130 135 140

Gln Pro Leu Val Phe Leu Tyr Glu Leu Leu Gln Val Glu Ala Pro Asn
145 150 155 160

Glu Tyr Gln Arg Glu Thr Trp Asn Leu Asn Asn Glu Glu Arg Met Gln
165 170 175

Ala Val Pro Leu Leu His Gly Glu Gly Asn Arg Leu Tyr Lys Leu Gly
180 185 190

Arg Tyr Asp Gln Ala Ala Thr Lys Tyr Gln Glu Ala Ile Val Cys Leu
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Glu Trp Leu Lys
210 215 220

Leu Glu Lys Met Ile Asn Thr Leu Ile Leu Asn Tyr Cys Gln Cys Leu
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Met Arg Ala Arg
260 265 270

Ala His Ala Glu Val Trp Asn Ala Glu Glu Ala Lys Ala Asp Leu Glu
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Arg Lys Ala Val Leu Arg Glu
290 295 300

Leu Arg Leu Leu Glu Ser Arg Leu Ala Asp Lys Gln Glu Glu Glu Arg
305 310 315 320

Gln Arg Cys Arg Ser Met Leu Gly
325

<210> 77
<211> 392
<212> PRT
<213> Macaca mulatta

<220>

UTHou-16UTL final.ST25

<221> peptide
<222> (1)..(392)
<223> Rhesus Monkey AILP1 Protein

<400> 77

Met Asp Ala Ala Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile
1 5 10 15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg
20 25 30

Val Ile Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val
35 40 45

Ile Asp Asp Ser Arg Gln Val Asp Gln Pro Met His Ile Ile Ile Gly
50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu Leu Thr Ser Met Arg
65 70 75 80

Val His Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val
85 90 95

Tyr Pro Ile Leu Ser Arg Ser Leu Arg Gln Met Ala Gln Gly Lys Asp
100 105 110

Pro Thr Glu Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala
115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro
130 135 140

Gln Pro Leu Ile Phe Val Ile Glu Leu Leu Gln Val Asp Ala Pro Ser
145 150 155 160

Asp Tyr Gln Arg Glu Thr Trp Asn Leu Ser Asn His Glu Lys Met Lys
165 170 175

Val Val Pro Val Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly
180 185 190

Arg Tyr Glu Glu Ala Ser Ser Lys Tyr Gln Glu Ala Ile Ile Cys Leu
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys

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210

215

220

Leu Glu Lys Met Ile Asn Thr Leu Thr Leu Asn Tyr Cys Gln Cys Leu
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg Ala Arg
260 265 270

Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala Asp Leu Gln
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Gln Lys Ala Val Arg Arg Glu
290 295 300

Leu Arg Leu Leu Glu Asn Arg Met Ala Glu Lys Gln Glu Glu Glu Arg
305 . . . 310 . . . 315 . . . 320

Leu Arg Cys Arg Asn Met Leu Ser Gln Gly Ala Thr Gln Pro Pro Ala
325 330 335

Glu Pro Pro Ala Gln Pro Pro Thr Ala Pro Pro Ala Glu Leu Ser Thr
340 345 350

Gly Pro Pro Ala Asp Pro Pro Ala Glu Pro Pro Thr Ala Pro Pro Ala
355 360 365

Glu Leu Ser Thr Gly Pro Pro Ala Glu Pro Pro Ala Glu Leu Pro Leu
370 375 380

Ser Pro Gly His Ser Leu Gln His
385 390

<210> 78
<211> 372
<212> PRT
<213> Saimiri sciureus

```
<220>
<221> peptide
<222> (1)..(372)
<223> Squirrel Monkey AIPL1 Protein
```

<400> 78

UTHou-16UTL final.ST25

Met Asp Ala Ala Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile
1 5 10 15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg
20 25 30

Val Ile Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val
35 40 45

Ile Asp Asp Ser Arg Glu Val Gly Gln Pro Met His Ile Ile Ile Gly
50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu Leu Thr Ser Met Arg
65 70 75 80

Val Arg Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val
85 90 95

Tyr Pro Ile Leu Ser Arg Ser Leu Arg Gln Met Ala Gln Gly Lys Asp
100 105 110

Pro Thr Glu Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala
115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro
130 135 140

Gln Pro Leu Ile Phe Val Ile Glu Leu Leu Gln Val Asp Ala Pro Ser
145 150 155 160

Asp Tyr Gln Arg Glu Thr Trp Asn Leu Ser Asn His Glu Lys Met Lys
165 170 175

Val Val Pro Val Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly
180 185 190

Arg Tyr Glu Glu Ala Ser Ser Lys Tyr Gln Glu Ala Ile Ile Cys Leu
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys
210 215 220

Leu Glu Lys Met Ile Asn Thr Leu Ile Leu Asn Tyr Cys Gln Cys Leu
225 230 235 240

UTHou-16UTL final.ST25

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg Ala Arg
260 265 270

Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala Asp Leu Gln
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Gln Lys Ala Val Arg Arg Glu
290 295 300

Leu Arg Leu Leu Glu Asn Arg Met Ala Glu Lys Gln Glu Glu Glu Arg
305 310 315 320

Leu Arg Cys Arg Asn Met Leu Ser Gln Gly Ala Thr Trp Ser Pro Ala
325 330 335

Glu Pro Pro Ala Glu Pro Pro Ala Glu Ser Ser Thr Glu Pro Pro Ala
340 345 350

Glu Pro Pro Ala Glu Pro Pro Ala Glu Leu Thr Leu Thr Pro Gly His
355 360 365

Pro Leu Gln His
370

<210> 79
<211> 328
<212> PRT
<213> Rattus norvegicus

<220>
<221> PEPTIDE
<222> (1)..(328)
<223> AIPL1 Protein rat - from Figure 1

<400> 79

Met Asp Ala Ala Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile
1 5 10 15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg
20 25 30

UTHou-16UTL final.ST25

Val Thr Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val
35 40 45

Ile Asp Asp Ser Lys Gln Val Gly Gln Pro Met Asn Ile Ile Ile Gly
50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu Leu Thr Ser Met Arg
65 70 75 80

Leu Gly Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val
85 90 95

Tyr Pro Met Leu Ser Arg Ser Leu Arg Gln Val Ala Glu Gly Lys Asp
100 105 110

Pro Thr Ser Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala
115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro
130 135 140

Gln Pro Leu Ile Phe Leu Ile Glu Leu Leu Gln Val Glu Ala Pro Asn
145 150 155 160

Glu Tyr Gln Arg Glu Thr Trp Asn Leu Asn Asn Glu Glu Arg Met Gln
165 170 175

Ala Val Pro Leu Leu His Gly Glu Gly Asn Arg Leu Tyr Lys Leu Gly
180 185 190

Arg Tyr Asp Gln Ala Ala Thr Lys Tyr Gln Glu Ala Ile Ile Cys Leu
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Glu Trp Leu Lys
210 215 220

Leu Glu Lys Met Ile Asn Thr Leu Ile Leu Asn Tyr Cys Gln Cys Leu
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Met Arg Ala Arg
260 265 270

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Ala His Ala Glu Val Trp Asn Ala Glu Glu Ala Lys Ala Asp Leu Glu
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Arg Lys Ala Val Leu Arg Glu
290 295 300

Leu Arg Leu Leu Glu Ser Arg Leu Ala Asp Lys Gln Glu Glu Glu Arg
305 310 315 320

Gln Arg Cys Arg Ser Met Leu Gly
325

<210> 80
<211> 330
<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE
<222> (1)..(330)
<223> AIP Protein human - From Figure 1

<400> 80

Met Ala Asp Ile Ile Ala Arg Leu Arg Glu Asp Gly Ile Gln Lys Arg
1 5 10 15

Val Ile Gln Glu Gly Arg Gly Glu Leu Pro Asp Phe Gln Asp Gly Thr
20 25 30

Lys Ala Thr Phe His Tyr Arg Thr Leu His Ser Asp Asp Glu Gly Thr
35 40 45

Val Leu Asp Asp Ser Arg Ala Arg Gly Lys Pro Met Glu Leu Ile Ile
50 55 60

Gly Lys Lys Phe Lys Leu Pro Val Trp Glu Thr Ile Val Cys Thr Met
65 70 75 80

Arg Glu Gly Glu Ile Ala Gln Phe Leu Cys Asp Ile Lys His Val Val
85 90 95

Leu Tyr Pro Leu Val Ala Lys Ser Leu Arg Asn Ile Ala Val Gly Lys
100 105 110

Asp Pro Leu Glu Gly Gln Arg His Cys Cys Gly Val Ala Gln Met Arg
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115

120

125

Glu His Ser Ser Leu Gly His Ala Asp Leu Asp Ala Leu Gln Gln Asn
 130 135 140

Pro Gln Pro Leu Ile Phe His Met Glu Met Leu Lys Val Glu Ser Pro
 145 150 155 160

Gly Thr Tyr Gln Gln Asp Pro Trp Ala Met Thr Asp Glu Glu Lys Ala
 165 170 175

Lys Ala Val Pro Leu Ile His Gln Glu Gly Asn Arg Leu Tyr Arg Glu
 180 185 190

Gly His Val Lys Glu Ala Ala Ala Lys Tyr Tyr Asp Ala Ile Ala Cys
 195 200 205

Leu Lys Asn Leu Gln Met Lys Glu Gln Pro Gly Ser Pro Glu Trp Ile
 210 215 220

Gln Leu Asp Lys Gln Ile Thr Pro Leu Leu Leu Asn Tyr Cys Gln Cys
 225 230 235 240

Lys Leu Val Val Glu Glu Tyr Tyr Glu Val Leu Asp His Cys Ser Ser
 245 250 255

Ile Leu Asn Lys Tyr Asp Asp Asn Val Lys Ala Tyr Phe Lys Arg Gly
 260 265 270

Lys Ala His Ala Ala Val Trp Asn Ala Gln Glu Ala Gln Ala Asp Phe
 275 280 285

Ala Lys Val Leu Glu Leu Asp Pro Ala Leu Ala Pro Val Val Ser Arg
 290 295 300

Glu Leu Arg Ala Leu Glu Ala Arg Ile Arg Gln Lys Asp Glu Glu Asp
 305 310 315 320

Lys Ala Arg Phe Arg Gly Ile Phe Ser His
 325 330

<210> 81
<211> 330
<212> PRT
<213> Mus musculus

UTHou-16UTL final.ST25

<220>
<221> PEPTIDE
<222> (1)..(330)
<223> AIP Protein mouse - From Figure 1

<400> 81

Met Ala Asp Leu Ile Ala Arg Leu Arg Glu Asp Gly Ile Gln Lys Arg
1 5 10 15

Val Ile Gln Glu Gly Arg Gly Glu Leu Pro Asp Phe Gln Asp Gly Thr
20 25 30

Lys Ala Thr Phe His Phe Arg Thr Leu His Ser Asp Asn Glu Gly Ser
35 40 45

Val Ile Asp Asp Ser Arg Thr Arg Gly Lys Pro Met Glu Leu Ile Val
50 55 60

Gly Lys Lys Phe Lys Leu Pro Val Trp Glu Thr Ile Val Cys Thr Met
65 70 75 80

Arg Glu Gly Glu Ile Ala Gln Phe Leu Cys Asp Ile Lys His Val Val
85 90 95

Leu Tyr Pro Leu Val Ala Lys Ser Leu Arg Asn Ile Ala Glu Gly Lys
100 105 110

Asp Pro Leu Glu Gly Gln Arg His Cys Cys Gly Ile Ala Gln Met His
115 120 125

Glu His Ser Ser Leu Gly His Ala Asp Leu Asp Ala Leu Gln Gln Asn
130 135 140

Pro Gln Pro Leu Ile Phe His Ile Glu Met Leu Lys Val Glu Ser Pro
145 150 155 160

Gly Thr Tyr Gln Gln Asp Pro Trp Ala Met Thr Asp Glu Glu Lys Ala
165 170 175

Lys Ala Val Pro Val Ile His Gln Glu Gly Asn Arg Leu Tyr Arg Glu
180 185 190

Gly Gln Val Lys Glu Ala Ala Lys Tyr Tyr Asp Ala Ile Ala Cys
195 200 205

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Leu Lys Asn Leu Gln Met Lys Glu Gln Pro Gly Ser Pro Asp Trp Ile
210 215 220

Gln Leu Asp Leu Gln Ile Thr Pro Leu Leu Leu Asn Tyr Cys Gln Cys
225 230 235 240

Lys Leu Val Ala Gln Glu Tyr Tyr Glu Val Leu Asp His Cys Ser Ser
245 250 255

Ile Leu Asn Lys Tyr Asp Asp Asn Val Lys Ala Tyr Phe Lys Arg Gly
260 265 270

Lys Ala His Ala Ala Val Trp Asn Ala Gln Glu Ala Gln Ala Asp Phe
275 280 285

Ala Lys Val Leu Glu Leu Asp Pro Ala Leu Ala Pro Val Val Ser Arg
290 295 300

Glu Leu Arg Ala Leu Glu Thr Arg Ile Arg Gln Lys Asp Glu Glu Asp
305 310 315 320

Lys Ala Arg Phe Arg Gly Ile Phe Ser His
325 330

<210> 82
<211> 8
<212> DNA
<213> Homo sapiens

<220>
<221> misc_structure
<222> (1)..(8)
<223> Eight Base insertion as Val 33 in the AIPL1 gene

<400> 82
gtgatctt

8

<210> 83
<211> 9
<212> DNA
<213> Homo sapiens

<220>
<221> misc_structure
<222> (1)..(9)
<223> Nine base deletion at Leu 257 of the AIPL1 gene

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<400> 83
ctccggcac

9